

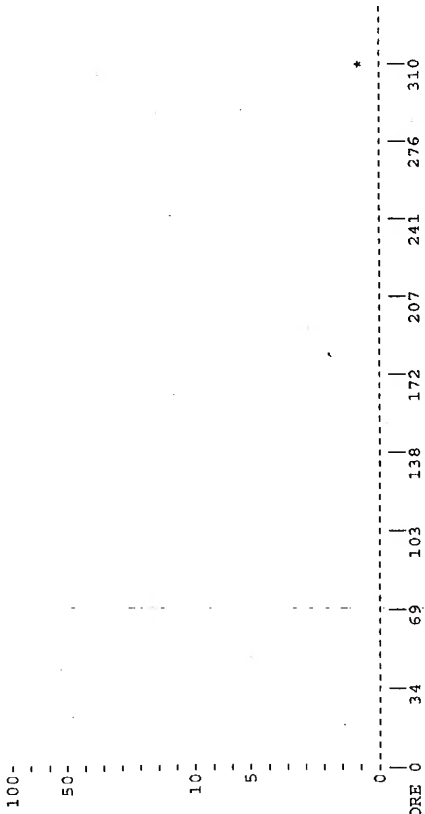
O < IntelliGenetics
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stDB - Fast Pairwise Comparison of Sequences
lease 5.4

sults file Seq140-aay87247.res made by tport on Wed 14 Jan 104 14:59:51-PST.

ery sequence being compared:US-10-006-485A-140 (1-311)
mber of sequences searched: 1
mber of scores above cutoff: 1

Results of the initial comparison of US-10-006-485A-140 (1-311) with:
File : aay87247.pep



PARAMETERS

ilarity matrix PAM-150 K-tuple 1
reshold level of sim. 16%
match penalty 1 Joining penalty 20
p penalty 5.00 Window size 311
p size penalty 0.05
loff score 1
ndomization group 0

SEARCH STATISTICS

cores: Mean Median Standard Deviation
310 0 0.00
mes: CPU 00:00:00.00 Total Elapsed 00:00:00.00
mber of residues: 311
mber of sequences searched: 1
mber of scores above cutoff: 1

re scores below are sorted by initial score.
ignificance is calculated based on initial score.
100% identical sequence to the query sequence was not found.

re list of best scores is:

Sequence Name Description Length Score Score Init. Opt. Sig. Frame

1. aay87247 Human signal peptide containi 311 310 310 0.00 0

1. US-10-006-485A-140 (1-311)
aay87247 Human signal peptide containing protein HSP-24 SE

Initial Score = 310 Optimized Score = 310 Significance = 0.00
Residue Identity = 99% Matches = 309 Mismatches = 1
Gaps = 0 Conservative Substitutions = 1

X 10 20 30 40 50 60 70
MGVPTALEAGSWRGSLLFALFLAASLGPVAAEKVATPYSLYVCPGQNVTLTCLLLGPVKGHDVTFYKTV
|||||
MGVPTALEAGSWRGSLLFALFLAASLGPVAAEKVATPYSLYVCPGQNVTLTCLLLGPVKGHDVTFYKTV
X 10 20 30 40 50 60 70
YSSRGEVQTCSERRPIRNLTFQDLHLHGGHQAANTSHDLAQHGLSESADHGFNFSITMRNLTLDSGLY
|||||
YSSRGEVQTCSERRPIRNLTFQDLHLHGGHQAANTSHDLAQHGLSESADHGFNFSITMRNLTLDSGLY
80 90 100 110 120 130 140
CCLVVEIRHHSEHRVHGAMELQVOTGKDPNSCVVYPSSQDSSENIATAALATGACIVGILCLPLLLVY
|||||
CCLVVEIRHHSEHRVHGAMELQVOTGKDPNSCVVYPSSQDSSENIATAALATGACIVGILCLPLLLVY
150 160 170 180 190 200 210
KQQAASNRRAQELVRMDSNIQGIENPGFEASPPAQGIPEAKVRHPLSYVACROPSESGRHLSPSTPLSP
|||||
KQQAASNRRAQELVRMDSNIQGIENPGFEASPPAQGIPEAKVRHPLSYVACROPSESGRHLSPSTPLSP
220 230 240 250 260 270 280
PGPGDVFFPSLDPVPDPSNFEVI
PGPGDVFFPSLDPVPDPSNFEVI
290 300 310